SEQUENCE LISTING

<110> Xu, Wenfeng
Kindsvogel, Wayne
Chandrasekher, Yasmin A.
Dillon, Stacey R.
Lehner, Joyce M.
Siadak, Anthony W.
Sivakumar, Pallavur V.
Moore, Margaret D.

<120> ANTI-IL-20 ANTIBODIES AND BINDING
PARTNERS AND METHODS OF USING IN INFLAMMATION

<130> 04-04

<150> US 60/457,481
<151> 2003-03-24

<150> US 60/523,295
<151> 2003-11-17

<160> 62

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2831
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (34)...(1755)

<400> 1
tagaggccaa gggagggctc tgtgccagcc ccg atg agg acg ctg ctg acc atc 54
Met Arg Thr Leu Leu Thr Ile
1 5

ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat 102
Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp
10 15 20

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg 150
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu
25 30 35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc 198
Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile
40 45 50 55

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt 246
Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys
60 65 70

cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac 294

```
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn
            75                  80                  85

ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc   342
Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly
        90                  95                  100

cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act   390
Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr
    105                 110                 115

acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att   438
Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile
120                 125                 130                 135

cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc   486
Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly
                140                 145                 150

cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta   534
His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu
            155                 160                 165

gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag   582
Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln
        170                 175                 180

aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc   630
Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly
    185                 190                 195

acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac   678
Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr
200                 205                 210                 215

atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc   726
Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe
                220                 225                 230

tcc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc   774
Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys
            235                 240                 245

tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc   822
Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser
        250                 255                 260

ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag   870
Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln
    265                 270                 275

gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg   918
Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu
280                 285                 290                 295

gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag   966
Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu
                300                 305                 310

ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta   1014
Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu
            315                 320                 325
```

```
ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc   1062
Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro
        330                 335                 340

cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc   1110
Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val
    345                 350                 355

ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca   1158
Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro
360                 365                 370                 375

ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc   1206
Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala
                380                 385                 390

cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg   1254
Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met
            395                 400                 405

gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa   1302
Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys
        410                 415                 420

cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc   1350
His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser
    425                 430                 435

tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg   1398
Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met
440                 445                 450                 455

gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc   1446
Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys
                460                 465                 470

aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg   1494
Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly
            475                 480                 485

aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag   1542
Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln
        490                 495                 500

atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca   1590
Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro
    505                 510                 515

tgt tcc ccc tcg gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc   1638
Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser
520                 525                 530                 535

ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca   1686
Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser
                540                 545                 550

gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc   1734
Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala
            555                 560                 565

ctg act gtg cag tgg gag tcc tgaggggaat gggaaaggct tggtgcttcc      1785
```

```
Leu Thr Val Gln Trp Glu Ser
        570

tccctgtccc tacccagtgt cacatccttg gctgtcaatc ccatgcctgc ccatgccaca 1845
cactctgcga tctggcctca gacgggtgcc cttgagagaa gcagagggag tggcatgcag 1905
ggcccctgcc atgggtgcgc tcctcaccgg aacaaagcag catgataagg actgcagcgg 1965
gggagctctg gggagcagct tgtgtagaca agcgcgtgct cgctgagccc tgcaaggcag 2025
aaatgacagt gcaaggagga aatgcaggga aactcccgag gtccagagcc ccacctccta 2085
acaccatgga ttcaaagtgc tcagggaatt tgcctctcct tgccccattc ctggccagtt 2145
tcacaatcta gctcgacaga gcatgaggcc cctgcctctt ctgtcattgt tcaaaggtgg 2205
gaagagagcc tggaaaagaa ccaggcctgg aaaagaacca gaaggaggct gggcagaacc 2265
agaacaacct gcacttctgc caaggccagg gccagcagga cggcaggact ctagggaggg 2325
gtgtggcctg cagctcattc ccagccaggg caactgcctg acgttgcacg atttcagctt 2385
cattcctctg atagaacaaa gcgaaatgca ggtccaccag ggagggagac acacaagcct 2445
tttctgcagg caggagtttc agaccctatc ctgagaatgg ggtttgaaag gaaggtgagg 2505
gctgtggccc ctggacgggt acaataacac actgtactga tgtcacaact ttgcaagctc 2565
tgccttgggt tcagcccatc tgggctcaaa ttccagcctc accactcaca agctgtgtga 2625
cttcaaacaa atgaaatcag tgcccagaac ctcggtttcc tcatctgtaa tgtggggatc 2685
ataacaccta cctcatggag ttgtggtgaa gatgaaatga agtcatgtct ttaaagtgct 2745
taatagtgcc tggtacatgg gcagtgccca ataaacggta gctatttaaa aaaaaaaaaa 2805
aaaaaaaaaa atagcggccg cctcga                                      2831

<210> 2
<211> 574
<212> PRT
<213> Homo sapiens

<400> 2
Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
 1               5                  10                  15
Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
            20                  25                  30
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
        35                  40                  45
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
    50                  55                  60
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
65                  70                  75                  80
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
                85                  90                  95
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
            100                 105                 110
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
        115                 120                 125
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
    130                 135                 140
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
145                 150                 155                 160
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
                165                 170                 175
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
            180                 185                 190
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
        195                 200                 205
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
    210                 215                 220
Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
225                 230                 235                 240
Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys
                245                 250                 255
Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
            260                 265                 270
```

```
Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
        275                 280                 285
Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile
    290                 295                 300
Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser
305                 310                 315                 320
Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln
                325                 330                 335
Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
            340                 345                 350
Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val
        355                 360                 365
Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys
    370                 375                 380
Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro
385                 390                 395                 400
Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr
                405                 410                 415
Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln
            420                 425                 430
Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
        435                 440                 445
Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
    450                 455                 460
His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
465                 470                 475                 480
Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
                485                 490                 495
Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
            500                 505                 510
Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
        515                 520                 525
Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
    530                 535                 540
Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp
545                 550                 555                 560
Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser
                565                 570
```

<210> 3
<211> 211
<212> PRT
<213> Homo sapiens

<400> 3

```
Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser Ser
 1               5                  10                  15
Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro
            20                  25                  30
Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
        35                  40                  45
Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
    50                  55                  60
Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
65                  70                  75                  80
Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
                85                  90                  95
Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
            100                 105                 110
Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
        115                 120                 125
```

```
Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
    130                 135                 140
Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
145                 150                 155                 160
His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
                165                 170                 175
Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
            180                 185                 190
Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
        195                 200                 205
Thr Trp Thr
    210


<210> 4
<211> 541
<212> PRT
<213> Artificial Sequence

<220>
<223> A Soluble IL-22RA-Fc Fusion Polypeptide

<400> 4
Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser Ser
 1               5                  10                  15
Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro
            20                  25                  30
Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
        35                  40                  45
Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
    50                  55                  60
Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
65                  70                  75                  80
Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
                85                  90                  95
Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
            100                 105                 110
Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
        115                 120                 125
Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
    130                 135                 140
Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
145                 150                 155                 160
His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
                165                 170                 175
Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
            180                 185                 190
Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
        195                 200                 205
Thr Trp Thr Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
    210                 215                 220
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
225                 230                 235                 240
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
                245                 250                 255
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
            260                 265                 270
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
        275                 280                 285
Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
    290                 295                 300
Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
```

```
305                 310                 315                 320
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
                325                 330                 335
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
            340                 345                 350
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
        355                 360                 365
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
    370                 375                 380
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
385                 390                 395                 400
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
                405                 410                 415
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
            420                 425                 430
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
        435                 440                 445
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
    450                 455                 460
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
465                 470                 475                 480
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
                485                 490                 495
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
            500                 505                 510
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
        515                 520                 525
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    530                 535                 540
```

<210> 5
<211> 1116
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (21)...(557)

<400> 5

```
tcgagttaga attgtctgca atg gcc gcc ctg cag aaa tct gtg agc tct ttc      53
                       Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe
                        1               5                   10

ctt atg ggg acc ctg gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg      101
Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu
             15                  20                  25

gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac      149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp
         30                  35                  40

aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg      197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu
     45                  50                  55

gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att      245
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
 60                  65                  70                  75

ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg      293
```

```
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu
                 80                  85                  90

atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa      341
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln
             95                 100                 105

tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc      389
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala
         110                 115                 120

agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg      437
Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu
     125                 130                 135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt      485
His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
140                 145                 150                 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt      533
Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe
                160                 165                 170

atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac     587
Met Ser Leu Arg Asn Ala Cys Ile
            175

taacccccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca    647
aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt    707
tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag actttctaag    767
catagatatt tattgataac atttcattgt aactggtgtt ctatacacag aaaacaattt    827
atttttttaaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa    887
aaacccctaa atagcttcat gtttccataa tcagtacttt atatttataa atgtatttat    947
tattattata agactgcatt ttatttatat cattttatta atatggattt atttatagaa   1007
acatcattcg atattgctac ttgagtgtaa ggctaatatt gatatttatg acaataatta   1067
tagagctata acatgtttat ttgacctcaa taaacacttg gatatccta               1116

<210> 6
<211> 179
<212> PRT
<213> Homo sapiens

<400> 6
Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu
 1               5                  10                  15
Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala
            20                  25                  30
Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
        35                  40                  45
Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
    50                  55                  60
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
65                  70                  75                  80
His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
                85                  90                  95
Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
            100                 105                 110
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
        115                 120                 125
Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
    130                 135                 140
Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
```

```
145                 150                 155                 160
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
                165                 170                 175
Ala Cys Ile
```

<210> 7
<211> 926
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (45)...(575)

<221> variation
<222> (188)...(188)
<223> Nucleotide may be C or G at position 188

<400> 7

```
ctttgaattc ctagctcctg tggtctccag atttcaggcc taag atg aaa gcc tct      56
                                                 Met Lys Ala Ser
                                                  1

agt ctt gcc ttc agc ctt ctc tct gct gcg ttt tat ctc cta tgg act      104
Ser Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
 5                   10                  15                  20

cct tcc act gga ctg aag aca ctc aat ttg gga agc tgt gtg atc gcc      152
Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile Ala
                25                  30                  35

aca aac ctt cag gaa ata cga aat gga ttt tct gas ata cgg ggc agt      200
Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Xaa Ile Arg Gly Ser
            40                  45                  50

gtg caa gcc aaa gat gga aac att gac atc aga atc tta agg agg act      248
Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu Arg Arg Thr
        55                  60                  65

gag tct ttg caa gac aca aag cct gcg aat cga tgc tgc ctc ctg cgc      296
Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys Cys Leu Leu Arg
    70                  75                  80

cat ttg cta aga ctc tat ctg gac agg gta ttt aaa aac tac cag acc      344
His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe Lys Asn Tyr Gln Thr
 85                  90                  95                 100

cct gac cat tat act ctc cgg aag atc agc agc ctc gcc aat tcc ttt      392
Pro Asp His Tyr Thr Leu Arg Lys Ile Ser Ser Leu Ala Asn Ser Phe
                105                 110                 115

ctt acc atc aag aag gac ctc cgg ctc tgt cat gcc cac atg aca tgc      440
Leu Thr Ile Lys Lys Asp Leu Arg Leu Cys His Ala His Met Thr Cys
            120                 125                 130

cat tgt ggg gag gaa gca atg aag aaa tac agc cag att ctg agt cac      488
His Cys Gly Glu Glu Ala Met Lys Lys Tyr Ser Gln Ile Leu Ser His
        135                 140                 145

ttt gaa aag ctg gaa cct cag gca gca gtt gtg aag gct ttg ggg gaa      536
```

```
Phe Glu Lys Leu Glu Pro Gln Ala Ala Val Val Lys Ala Leu Gly Glu
    150                 155                 160

cta gac att ctt ctg caa tgg atg gag gag aca gaa tag gaggaaagtg       585
Leu Asp Ile Leu Leu Gln Trp Met Glu Glu Thr Glu  *
165                 170                 175

atgctgctgc taagaatatt cgaggtcaag agctccagtc ttcaatacct gcagaggagg    645
catgacccca aaccaccatc tctttactgt actagtcttg tgctggtcac agtgtatctt    705
atttatgcat tacttgcttc cttgcatgat tgtctttatg catccccaat cttaattgag    765
accatacttg tataagattt ttgtaatatc tttctgctat tggatatatt tattagttaa    825
tatatttatt tatttttgc tattaatgta tttaattttt tacttgggca tgaaacttta    885
aaaaaaattc acaagattat atttataacc tgactagagc a                       926

<210> 8
<211> 176
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (48)...(48)
<223> Amino acid at position 48 can be a D (Asp) or E
      (Glu)

<221> VARIANT
<222> 48
<223> Xaa = Any Amino Acid

<400> 8
Met Lys Ala Ser Ser Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr
 1               5                  10                  15
Leu Leu Trp Thr Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser
            20                  25                  30
Cys Val Ile Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Xaa
        35                  40                  45
Ile Arg Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile
    50                  55                  60
Leu Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
65                  70                  75                  80
Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe Lys
                85                  90                  95
Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser Ser Leu
            100                 105                 110
Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu Cys His Ala
        115                 120                 125
His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys Lys Tyr Ser Gln
    130                 135                 140
Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln Ala Ala Val Val Lys
145                 150                 155                 160
Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln Trp Met Glu Glu Thr Glu
                165                 170                 175


<210> 9
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide Linker
```

<400> 9
Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15

<210> 10
<211> 1050
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (5)...(589)

<400> 10
aaca ggc tct cct ctc act tat caa ctt ttg aca ctt gtg cga tcg gtg   49
     Gly Ser Pro Leu Thr Tyr Gln Leu Leu Thr Leu Val Arg Ser Val
      1   5   10   15

atg gct gtc ctg cag aaa tct atg agt ttt tcc ctt atg ggg act ttg   97
Met Ala Val Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu
                 20   25   30

gcc gcc agc tgc ctg ctt ctc att gcc ctg tgg gcc cag gag gca aat   145
Ala Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn
             35   40   45

gcg ctg ccc atc aac acc cgg tgc aag ctt gag gtg tcc aac ttc cag   193
Ala Leu Pro Ile Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln
         50   55   60

cag ccg tac atc gtc aac cgc acc ttt atg ctg gcc aag gag gcc agc   241
Gln Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
     65   70   75

ctt gca gat aac aac aca gac gtc cgg ctc atc ggg gag aaa ctg ttc   289
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 80   85   90   95

cga gga gtc agt gct aag gat cag tgc tac ctg atg aag cag gtg ctc   337
Arg Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu
                100   105   110

aac ttc acc ctg gaa gac att ctg ctc ccc cag tca gac agg ttc cgg   385
Asn Phe Thr Leu Glu Asp Ile Leu Leu Pro Gln Ser Asp Arg Phe Arg
            115   120   125

ccc tac atg cag gag gtg gtg cct ttc ctg acc aaa ctc agc aat cag   433
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln
        130   135   140

ctc agc tcc tgt cac atc agt ggt gac gac cag aac atc cag aag aat   481
Leu Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn
    145   150   155

gtc aga agg ctg aag gag aca gtg aaa aag ctt gga gag agc gga gag   529
Val Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
160   165   170   175

atc aaa gcg atc ggg gaa ctg gac ctg ctg ttt atg tct ctg aga aat   577
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
                180   185   190

```
gct tgc gtc tga gcgagaagaa gctagaaaac gaagaactgc tccttcctgc          629
Ala Cys Val  *


cttctaaaaa gaacaataag atccctgaat ggacttttt actaaaggaa agtgagaagc    689
taacgtccac catcattaga agatttcaca tgaaacctgg ctcagttgaa agagaaaata    749
gtgtcaagtt gtccatgaga ccagaggtag acttgataac cacaaagatt cattgacaat    809
attttattgt cattgataat gcaacagaaa aagtatgtac tttaaaaaat tgtttgaaag    869
gaggttacct ctcattcctc tagaagaaaa gcctatgtaa cttcatttcc ataaccaata    929
ctttatatat gtaagtttat ttattataag tatacatttt atttatgtca gtttattaat    989
atggatttat ttatagaaaa attatctgat gttgatattt gagtataaag caaataatat   1049
t                                                                   1050

<210> 11
<211> 194
<212> PRT
<213> Mus musculus

<400> 11
Gly Ser Pro Leu Thr Tyr Gln Leu Leu Thr Leu Val Arg Ser Val Met
 1               5                  10                  15
Ala Val Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu Ala
            20                  25                  30
Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn Ala
        35                  40                  45
Leu Pro Ile Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln Gln
    50                  55                  60
Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
65                  70                  75                  80
Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe Arg
                85                  90                  95
Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu Asn
            100                 105                 110
Phe Thr Leu Glu Asp Ile Leu Leu Pro Gln Ser Asp Arg Phe Arg Pro
        115                 120                 125
Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln Leu
    130                 135                 140
Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn Val
145                 150                 155                 160
Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile
                165                 170                 175
Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala
            180                 185                 190
Cys Val



<210> 12
<211> 2149
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(693)

<400> 12
atg atg cct aaa cat tgc ttt cta ggc ttc ctc atc agt ttc ttc ctt       48
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 1               5                  10                  15
```

```
act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag        96
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
             20                  25                  30

agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag       144
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
         35                  40                  45

cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac       192
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
     50                  55                  60

aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt       240
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65                  70                  75                  80

act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag       288
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
                 85                  90                  95

gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca       336
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
            100                 105                 110

gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata       384
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
        115                 120                 125

gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta       432
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
    130                 135                 140

att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat       480
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145                 150                 155                 160

gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att       528
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
                165                 170                 175

aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga       576
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
            180                 185                 190

gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg       624
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
        195                 200                 205

gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa       672
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
    210                 215                 220

gag aga tgt gtg gaa att cca tgacttgtgg aatttggcat tcagcaatgt          723
Glu Arg Cys Val Glu Ile Pro
225                 230

ggaaattcta aagctccctg agaacaggat gactcgtgtt tgaaggatct tatttaaaat    783
tgtttttgta ttttcttaaa gcaatattca ctgttacacc ttggggactt ctttgtttat    843
ccattctttt atcctttata tttcatttta aactatattt gaacgacatt ccccccgaaa    903
aattgaaatg taaagatgag gcagagaata aagtgttcta tgaaattcag aactttattt    963
ctgaatgtaa catccctaat aacaaccttc attcttctaa tacagcaaaa taaaaattta   1023
acaaccaagg aatagtattt aagaaaatgt tgaaataatt tttttaaaat agcattacag   1083
```

```
actgaggcgg tcctgaagca atggtttttc actctcttat tgagccaatt aaattgacat   1143
tgctttgaca atttaaaact tctataaagg tgaatatttt tcatacattt ctattttata   1203
tgaatatact ttttatatat ttattattat taaatatttc tacttaatga atcaaaattt   1263
tgttttaaag tctactttat gtaaataaga acaggttttg gggaaaaaaa tcttatgatt   1323
tctggattga tatctgaatt aaaactatca acaacaagga agtctactct gtacaattgt   1383
ccctcattta aaagatatat taagctttc ttttctgttt gtttttgttt tgtttagttt   1443
ttaatcctgt cttagaagaa cttatcttta ttctcaaaat taaatgtaat ttttttagtg   1503
acaaagaaga aaggaaacct cattactcaa tccttctggc caagagtgtc ttgcttgtgg   1563
cgccttcctc atctctatat aggaggatcc catgaatgat ggtttattgg gaactgctgg   1623
ggtcgacccc atacagagaa ctcagcttga agctggaagc acacagtggg tagcaggaga   1683
aggaccggtg ttggtaggtg cctacagaga ctatagagct agacaaagcc ctccaaactg   1743
gcccctcctg ctcactgcct ctcctgagta gaaatctggt gacctaaggc tcagtgcggt   1803
caacagaaag ctgccttctt cacttgaggc taagtcttca tatatgttta aggttgtctt   1863
tctagtgagg agatacatat cagagaacat ttgtacaatt ccccatgaaa attgctccaa   1923
agttgataac aatatagtcg gtgcttctag ttatatgcaa gtactcagtg ataaatggat   1983
taaaaaatat tcagaaatgt attgggggt ggaggagaat aagaggcaga gcaagagcta   2043
gagaattggt ttccttgctt ccctgtatgc tcagaaaaca ttgatttgag catagacgca   2103
gagactgaaa aaaaaaaaat gctcgagcgg ccgccatatc cttggt                  2149
```

<210> 13
<211> 231
<212> PRT
<213> Homo sapiens

<400> 13

```
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 1               5                  10                  15
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
            20                  25                  30
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
        35                  40                  45
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
    50                  55                  60
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65                  70                  75                  80
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
                85                  90                  95
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
            100                 105                 110
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
        115                 120                 125
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
    130                 135                 140
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145                 150                 155                 160
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
                165                 170                 175
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
            180                 185                 190
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
        195                 200                 205
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
    210                 215                 220
Glu Arg Cys Val Glu Ile Pro
225                 230
```

<210> 14
<211> 699
<212> DNA
<213> Artificial Sequence

<220>
<223> C-Terminal Fc4 tag

<400> 14
gagcccagat cttcagacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgag 60
ggggcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaaataa 699

<210> 15
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Glu-Glu (CEE) Peptide Tag

<400> 15
Glu Tyr Met Pro Met Glu
1 5

<210> 16
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Glu-Glu (CEE) Peptide Tag with spacer

<400> 16
Gly Ser Gly Gly Glu Tyr Met Pro Met Glu
1 5 10

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39289

<400> 17
tccgaggagt caatgctaag 20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer ZC39290

<400> 18
tccaagcttt ttcactgtct 20

<210> 19
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer ZC39776

<400> 19
gggcccgcta gcacct 16

<210> 20
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer ZC39777

<400> 20
gggtgatccg ctggca 16

<210> 21
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-20 FAM/TAMRA labeled TaqMan probe ZC38752

<400> 21
ccagccactt tctctctccg tatttcttat attcca 36

<210> 22
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer, ZC42459

<400> 22
tggccaggct cagcaa 16

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer, ZC42458

<400> 23
gcacattcct ctggatatgc a 21

<210> 24
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-22 TaqMan probe, ZC42460

<400> 24
aggctaagca catgtcatat tgaaggtgat g 31

<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer, ZC40541

<400> 25
tcgccaattc ctttcttacc a 21

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer, ZC40542

<400> 26
cccacaatgg catgtcatgt 20

<210> 27
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-20 TaqMan® probe ZC40544

<400> 27
agaaggacct ccggctctgt catgc 25

<210> 28
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC45,593

<400> 28
caggaaatcc atgccgagtt gagacgcttc cgtagacacg cccctgagga cccctcg 57

<210> 29
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC45,592

<400> 29
tctgggctca ccgcttccag acccgcttcc agacccgctt cctgtccggt ctggcagtgt 60
ctt 63

<210> 30
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC45,591

<400> 30
gaccggacag gaagcgggtc tggaagcggg tctggaagcg gtgagcccag aggccccaca 60
atc 63

<210> 31
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC45,594

<400> 31
agagctgttt taaggcgcgc ctctagatta tttttattta cccggagtcc gggagaa 57

<210> 32
<211> 531
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(531)

<400> 32
atg aaa ggc ttt ggt ctt gcc ttt gga ctg ttc tcc gct gtg ggt ttt 48
Met Lys Gly Phe Gly Leu Ala Phe Gly Leu Phe Ser Ala Val Gly Phe
1 5 10 15

ctt ctc tgg act cct tta act ggg ctc aag acc ctc cat ttg gga agc 96
Leu Leu Trp Thr Pro Leu Thr Gly Leu Lys Thr Leu His Leu Gly Ser
20 25 30

tgt gtg att act gca aac cta cag gca ata caa aag gaa ttt tct gag 144
Cys Val Ile Thr Ala Asn Leu Gln Ala Ile Gln Lys Glu Phe Ser Glu
35 40 45

att cgg gat agt gtg caa gct gaa gat aca aat att gac atc aga att 192
Ile Arg Asp Ser Val Gln Ala Glu Asp Thr Asn Ile Asp Ile Arg Ile
50 55 60

tta agg acg act gag tct ttg aaa gac ata aag tct ttg gat agg tgc 240
Leu Arg Thr Thr Glu Ser Leu Lys Asp Ile Lys Ser Leu Asp Arg Cys
65 70 75 80

tgc ttc ctt cgt cat cta gtg aga ttc tat ctg gac agg gta ttc aaa 288
Cys Phe Leu Arg His Leu Val Arg Phe Tyr Leu Asp Arg Val Phe Lys
85 90 95

gtc tac cag acc cct gac cac cat acc ctg aga aag atc agc agc ctc 336
Val Tyr Gln Thr Pro Asp His His Thr Leu Arg Lys Ile Ser Ser Leu
100 105 110

```
gcc aac tcc ttt ctt atc atc aag aag gac ctc tca gtc tgt cat tct   384
Ala Asn Ser Phe Leu Ile Ile Lys Lys Asp Leu Ser Val Cys His Ser
        115                 120                 125

cac atg gca tgt cat tgt ggg gaa gaa gca atg gag aaa tac aac caa   432
His Met Ala Cys His Cys Gly Glu Glu Ala Met Glu Lys Tyr Asn Gln
    130                 135                 140

att ctg agt cac ttc ata gag ttg gaa ctt cag gca gcg gtg gta aag   480
Ile Leu Ser His Phe Ile Glu Leu Glu Leu Gln Ala Ala Val Val Lys
145                 150                 155                 160

gct ttg gga gaa cta ggc att ctt ctg aga tgg atg gag gag atg cta   528
Ala Leu Gly Glu Leu Gly Ile Leu Leu Arg Trp Met Glu Glu Met Leu
                165                 170                 175

tag                                                               531
 *
```

<210> 33
<211> 176
<212> PRT
<213> Mus musculus

<400> 33

```
Met Lys Gly Phe Gly Leu Ala Phe Gly Leu Phe Ser Ala Val Gly Phe
 1               5                  10                  15
Leu Leu Trp Thr Pro Leu Thr Gly Leu Lys Thr Leu His Leu Gly Ser
            20                  25                  30
Cys Val Ile Thr Ala Asn Leu Gln Ala Ile Gln Lys Glu Phe Ser Glu
        35                  40                  45
Ile Arg Asp Ser Val Gln Ala Glu Asp Thr Asn Ile Asp Ile Arg Ile
    50                  55                  60
Leu Arg Thr Thr Glu Ser Leu Lys Asp Ile Lys Ser Leu Asp Arg Cys
65                  70                  75                  80
Cys Phe Leu Arg His Leu Val Arg Phe Tyr Leu Asp Arg Val Phe Lys
                85                  90                  95
Val Tyr Gln Thr Pro Asp His His Thr Leu Arg Lys Ile Ser Ser Leu
            100                 105                 110
Ala Asn Ser Phe Leu Ile Ile Lys Lys Asp Leu Ser Val Cys His Ser
        115                 120                 125
His Met Ala Cys His Cys Gly Glu Glu Ala Met Glu Lys Tyr Asn Gln
    130                 135                 140
Ile Leu Ser His Phe Ile Glu Leu Glu Leu Gln Ala Ala Val Val Lys
145                 150                 155                 160
Ala Leu Gly Glu Leu Gly Ile Leu Leu Arg Trp Met Glu Glu Met Leu
                165                 170                 175
```

<210> 34
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC22901

<400> 34
catcaaaccg cctgatgtga c 21

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC45039

<400> 35
attaggcttg ggagggaatg g 21

<210> 36
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC38573

<400> 36
tggcgatgcc tgcttgccga ata 23

<210> 37
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC25223

<400> 37
gtcttcctca catctgttat cg 22

<210> 38
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC40128

<400> 38
ggcttgaact ttgagaaagg cagt 24

<210> 39
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-22RA Extracellular domain with tPA leader and
fused to murine gamma 2a heavy chain Fc region
(mG2a)

<221> CDS
<222> (1)...(1473)

<400> 39
atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt ggc 48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

```
gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc gag ttg aga cgc   96
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
            20                  25                  30

ttc cgt aga cac gcc cct gag gac ccc tcg gat ctg ctc cag cac gtg   144
Phe Arg Arg His Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val
        35                  40                  45

aaa ttc cag tcc agc aac ttt gaa aac atc ctg acg tgg gac agc ggg   192
Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly
    50                  55                  60

cca gag ggc acc cca gac acg gtc tac agc atc gag tat aag acg tac   240
Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr
65                  70                  75                  80

gga gag agg gac tgg gtg gca aag aag ggc tgt cag cgg atc acc cgg   288
Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg
                85                  90                  95

aag tcc tgc aac ctg acg gtg gag acg ggc aac ctc acg gag ctc tac   336
Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr
            100                 105                 110

tat gcc agg gtc acc gct gtc agt gcg gga ggc cgg tca gcc acc aag   384
Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys
        115                 120                 125

atg act gac agg ttc agc tct ctg cag cac act acc ctc aag cca cct   432
Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro
    130                 135                 140

gat gtg acc tgt atc tcc aaa gtg aga tcg att cag atg att gtt cat   480
Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His
145                 150                 155                 160

cct acc ccc acg cca atc cgt gca ggc gat ggc cac cgg cta acc ctg   528
Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu
                165                 170                 175

gaa gac atc ttc cat gac ctg ttc tac cac tta gag ctc cag gtc aac   576
Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn
            180                 185                 190

cgc acc tac caa atg cac ctt gga ggg aag cag aga gaa tat gag ttc   624
Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe
        195                 200                 205

ttc ggc ctg acc cct gac aca gag ttc ctt ggc acc atc atg att tgc   672
Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys
    210                 215                 220

gtt ccc acc tgg gcc aag gag agt gcc ccc tac atg tgc cga gtg aag   720
Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys
225                 230                 235                 240

aca ctg cca gac cgg aca gga agc ggg tct gga agc ggg tct gga agc   768
Thr Leu Pro Asp Arg Thr Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
                245                 250                 255

ggt gag ccc aga ggc ccc aca atc aag ccc tgt cct cca tgc aaa tgc   816
Gly Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
```

```
            260                 265                 270

cca gca cct aac ctc ttg ggt gga cca tcc gtc ttc atc ttc cct cca   864
Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
        275                 280                 285

aag atc aag gat gta ctc atg atc tcc ctg agc ccc ata gtc aca tgt   912
Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
    290                 295                 300

gtg gtg gtg gat gtg agc gag gat gac cca gat gtc cag atc agc tgg   960
Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
305                 310                 315                 320

ttt gtg aac aac gtg gaa gta cac aca gct cag aca caa acc cat aga   1008
Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
                325                 330                 335

gag gat tac aac agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag   1056
Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
            340                 345                 350

cac cag gac tgg atg agt ggc aag gag ttc aaa tgc aag gtc aac aac   1104
His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
        355                 360                 365

aaa gac ctc cca gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg   1152
Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly
    370                 375                 380

tca gta aga gct cca cag gta tat gtc ttg cct cca cca gaa gaa gag   1200
Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu
385                 390                 395                 400

atg act aag aaa cag gtc act ctg acc tgc atg gtc aca gac ttc atg   1248
Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
                405                 410                 415

cct gaa gac att tac gtg gag tgg acc aac aac ggg aaa aca gag cta   1296
Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
            420                 425                 430

aac tac aag aac act gaa cca gtc ctg gac tct gat ggt tct tac ttc   1344
Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe
        435                 440                 445

atg tac agc aag ctg aga gtg gaa aag aag aac tgg gtg gaa aga aat   1392
Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
    450                 455                 460

agc tac tcc tgt tca gtg gtc cac gag ggt ctg cac aat cac cac acg   1440
Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
465                 470                 475                 480

act aag agc ttc tcc cgg act ccg ggt aaa taa                      1473
Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys  *
                485                 490
```

<210> 40
<211> 490
<212> PRT

<213> Artificial Sequence

<220>
<223> IL-22RA Extracellular domain with tPA leader and fused to murine gamma 2a heavy chain Fc region (mG2a)

<400> 40

```
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1               5                  10                  15
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
            20                  25                  30
Phe Arg Arg His Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val
        35                  40                  45
Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly
    50                  55                  60
Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr
65                  70                  75                  80
Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg
                85                  90                  95
Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr
            100                 105                 110
Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys
        115                 120                 125
Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro
    130                 135                 140
Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His
145                 150                 155                 160
Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu
                165                 170                 175
Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn
            180                 185                 190
Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe
        195                 200                 205
Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys
    210                 215                 220
Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys
225                 230                 235                 240
Thr Leu Pro Asp Arg Thr Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
                245                 250                 255
Gly Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
            260                 265                 270
Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
        275                 280                 285
Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
    290                 295                 300
Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
305                 310                 315                 320
Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
                325                 330                 335
Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
            340                 345                 350
His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
        355                 360                 365
Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly
    370                 375                 380
Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu
385                 390                 395                 400
Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
                405                 410                 415
Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
            420                 425                 430
```

```
Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe
        435                 440                 445
Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
    450                 455                 460
Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
465                 470                 475                 480
Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
                485                 490


<210> 41
<211> 1834
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (43)...(1788)

<400> 41
ttggtccaga gccgaggccc gaaggggccc tggagggacc ca atg aag aca cta    54
                                              Met Lys Thr Leu
                                               1

ctg acc atc ctg acg gtg gga tcc ctg gcc gct cac acc act gtg gac   102
Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His Thr Thr Val Asp
 5                   10                  15                  20

aca tcc ggt ctc ctt caa cac gtg aaa ttc cag tcc agc aac ttt gag   150
Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu
                25                  30                  35

aac atc ttg acg tgg gat ggt ggg ccc gct agc acc tct gac acc gtc   198
Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser Thr Ser Asp Thr Val
            40                  45                  50

tac agt gtg gaa tat aag aaa tac gga gag aga aag tgg ctg gcc aag   246
Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg Lys Trp Leu Ala Lys
        55                  60                  65

gcg ggc tgc cag cgg atc acc cag aag ttc tgc aac ctg act atg gag   294
Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys Asn Leu Thr Met Glu
    70                  75                  80

acc cgc aac cac act gag ttt tac tac gcc aag gtc acg gca gtc agc   342
Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys Val Thr Ala Val Ser
 85                  90                  95                  100

gca gga ggc cca cca gtc aca aag atg act gat cgt ttc agc tcg ctg   390
Ala Gly Gly Pro Pro Val Thr Lys Met Thr Asp Arg Phe Ser Ser Leu
                105                 110                 115

cag cac act acc atc aaa ccg cct gat gtg acc tgt atc ccc aaa gtg   438
Gln His Thr Thr Ile Lys Pro Pro Asp Val Thr Cys Ile Pro Lys Val
            120                 125                 130

agg tcc att cag atg ctg gtc cac ccc aca ctc aca ccg gtc ctc tcg   486
Arg Ser Ile Gln Met Leu Val His Pro Thr Leu Thr Pro Val Leu Ser
        135                 140                 145

gaa gat ggc cac cag cta acc ctg gag gag att ttc cat gac ctg ttc   534
Glu Asp Gly His Gln Leu Thr Leu Glu Glu Ile Phe His Asp Leu Phe
```

```
    150                 155                 160

tac cgc tta gag ctc cac gtc aac cac acc tac cag atg cac ctt gaa   582
Tyr Arg Leu Glu Leu His Val Asn His Thr Tyr Gln Met His Leu Glu
165                 170                 175                 180

ggc aaa cag aga gaa tac gag ttc ctt ggc ctg act ccc gac aca gag   630
Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu Thr Pro Asp Thr Glu
                185                 190                 195

ttc ctc ggc tcc atc aca att ttg act ccg ata ttg tcc aag gaa agt   678
Phe Leu Gly Ser Ile Thr Ile Leu Thr Pro Ile Leu Ser Lys Glu Ser
            200                 205                 210

gcc ccc tac gtg tgc cga gtg aag acg ctg ccc gat cgg acg tgg gcc   726
Ala Pro Tyr Val Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Ala
        215                 220                 225

tac tcc ttc tcg ggc gcc gtg ctc ttt tcc atg ggt ttc ctc gtc ggc   774
Tyr Ser Phe Ser Gly Ala Val Leu Phe Ser Met Gly Phe Leu Val Gly
    230                 235                 240

ttg ctc tgt tat ctg ggc tac aaa tac atc acc aag cca cct gta cct   822
Leu Leu Cys Tyr Leu Gly Tyr Lys Tyr Ile Thr Lys Pro Pro Val Pro
245                 250                 255                 260

cct aac tcc ctg aac gtc caa cgt gtc ctg acc ttt caa ccc cta cgc   870
Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg
                265                 270                 275

ttc atc caa gaa cac gta ctg atc cct gtc ttg gac ctc agt ggc ccc   918
Phe Ile Gln Glu His Val Leu Ile Pro Val Leu Asp Leu Ser Gly Pro
            280                 285                 290

agc agt ctg cct cag ccc atc cag tac tcc caa gtg gtg gtg tct ggg   966
Ser Ser Leu Pro Gln Pro Ile Gln Tyr Ser Gln Val Val Val Ser Gly
        295                 300                 305

ccc agg gag cct cct gga gct gtg tgg cgg cag agc ctg tct gac ctc  1014
Pro Arg Glu Pro Pro Gly Ala Val Trp Arg Gln Ser Leu Ser Asp Leu
    310                 315                 320

acc tac gta ggg cag tca gat gtc tcc atc ctg caa cct acc aac gtg  1062
Thr Tyr Val Gly Gln Ser Asp Val Ser Ile Leu Gln Pro Thr Asn Val
325                 330                 335                 340

cca gct cag cag aca ctg tcc cca cca tcc tac gct ccg aag gct gtc  1110
Pro Ala Gln Gln Thr Leu Ser Pro Pro Ser Tyr Ala Pro Lys Ala Val
                345                 350                 355

cct gag gtc cag ccc cct tcc tat gcg cct cag gta gcc tcg gat gcc  1158
Pro Glu Val Gln Pro Pro Ser Tyr Ala Pro Gln Val Ala Ser Asp Ala
            360                 365                 370

aaa gct ctg ttc tac tca cca caa cag ggg atg aag acc agg cct gcc  1206
Lys Ala Leu Phe Tyr Ser Pro Gln Gln Gly Met Lys Thr Arg Pro Ala
        375                 380                 385

acc tat gac ccg cag gac att ctg gac agc tgc cct gct tct tat gct  1254
Thr Tyr Asp Pro Gln Asp Ile Leu Asp Ser Cys Pro Ala Ser Tyr Ala
    390                 395                 400
```

```
gtg tgt gtg gaa gac tct ggc aaa gac tct acc cca ggc atc ctc tcc   1302
Val Cys Val Glu Asp Ser Gly Lys Asp Ser Thr Pro Gly Ile Leu Ser
405                 410                 415                 420

act ccc aaa tac ctc aag aca aaa ggt cag ctc cag gaa gac aca ctt   1350
Thr Pro Lys Tyr Leu Lys Thr Lys Gly Gln Leu Gln Glu Asp Thr Leu
                425                 430                 435

gtt aga agc tgt ctc cca ggg gac ctt tct cta cag aaa gtc acc tcc   1398
Val Arg Ser Cys Leu Pro Gly Asp Leu Ser Leu Gln Lys Val Thr Ser
            440                 445                 450

tta ggt gaa ggg gag aca cag aga cca aaa tca ctc ccc tca cct ctg   1446
Leu Gly Glu Gly Glu Thr Gln Arg Pro Lys Ser Leu Pro Ser Pro Leu
        455                 460                 465

gga ttt tgc aca gac aga gga cct gac ctt cac aca ctg cgc agt gag   1494
Gly Phe Cys Thr Asp Arg Gly Pro Asp Leu His Thr Leu Arg Ser Glu
    470                 475                 480

gaa cca gag aca cca cgg tac ctg aag ggg gcg ctg tct ctc ctg tcc   1542
Glu Pro Glu Thr Pro Arg Tyr Leu Lys Gly Ala Leu Ser Leu Leu Ser
485                 490                 495                 500

tct gtg cag atc gag ggc cac cct gtc tcc ctc cct ttg cac gtc cat   1590
Ser Val Gln Ile Glu Gly His Pro Val Ser Leu Pro Leu His Val His
                505                 510                 515

tct gtc tca tgt tcc ccc tca gac gag gga cca agt ccc tgg ggc ctg   1638
Ser Val Ser Cys Ser Pro Ser Asp Glu Gly Pro Ser Pro Trp Gly Leu
            520                 525                 530

ctg gac tcc ctt gtg tgt cca aag gat gag ggt ccc gcg gtt gag act   1686
Leu Asp Ser Leu Val Cys Pro Lys Asp Glu Gly Pro Ala Val Glu Thr
        535                 540                 545

gag gcc atg tgc ccc agt gct gca gcc tct gag ctg gag cag tcc aca   1734
Glu Ala Met Cys Pro Ser Ala Ala Ala Ser Glu Leu Glu Gln Ser Thr
    550                 555                 560

gaa ctg gac tct ctt ttc aaa ggc ttg gcc ctg act gtg cag tgg gaa   1782
Glu Leu Asp Ser Leu Phe Lys Gly Leu Ala Leu Thr Val Gln Trp Glu
565                 570                 575                 580

tcc tga agggagatcg gagcaagcag gcctaagttt cctcccgccc caccta        1834
Ser  *
```

<210> 42
<211> 581
<212> PRT
<213> Mus musculus

<400> 42

```
Met Lys Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
 1               5                  10                  15
Thr Thr Val Asp Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln Ser
            20                  25                  30
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser Thr
        35                  40                  45
Ser Asp Thr Val Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg Lys
```

```
    50                  55                  60
Trp Leu Ala Lys Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys Asn
65                  70                  75                  80
Leu Thr Met Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys Val
                85                  90                  95
Thr Ala Val Ser Ala Gly Gly Pro Pro Val Thr Lys Met Thr Asp Arg
            100                 105                 110
Phe Ser Ser Leu Gln His Thr Thr Ile Lys Pro Pro Asp Val Thr Cys
        115                 120                 125
Ile Pro Lys Val Arg Ser Ile Gln Met Leu Val His Pro Thr Leu Thr
    130                 135                 140
Pro Val Leu Ser Glu Asp Gly His Gln Leu Thr Leu Glu Glu Ile Phe
145                 150                 155                 160
His Asp Leu Phe Tyr Arg Leu Glu Leu His Val Asn His Thr Tyr Gln
                165                 170                 175
Met His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu Thr
            180                 185                 190
Pro Asp Thr Glu Phe Leu Gly Ser Ile Thr Ile Leu Thr Pro Ile Leu
        195                 200                 205
Ser Lys Glu Ser Ala Pro Tyr Val Cys Arg Val Lys Thr Leu Pro Asp
    210                 215                 220
Arg Thr Trp Ala Tyr Ser Phe Ser Gly Ala Val Leu Phe Ser Met Gly
225                 230                 235                 240
Phe Leu Val Gly Leu Leu Cys Tyr Leu Gly Tyr Lys Tyr Ile Thr Lys
                245                 250                 255
Pro Pro Val Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
            260                 265                 270
Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Leu Asp
        275                 280                 285
Leu Ser Gly Pro Ser Ser Leu Pro Gln Pro Ile Gln Tyr Ser Gln Val
    290                 295                 300
Val Val Ser Gly Pro Arg Glu Pro Pro Gly Ala Val Trp Arg Gln Ser
305                 310                 315                 320
Leu Ser Asp Leu Thr Tyr Val Gly Gln Ser Asp Val Ser Ile Leu Gln
                325                 330                 335
Pro Thr Asn Val Pro Ala Gln Gln Thr Leu Ser Pro Pro Ser Tyr Ala
            340                 345                 350
Pro Lys Ala Val Pro Glu Val Gln Pro Pro Ser Tyr Ala Pro Gln Val
        355                 360                 365
Ala Ser Asp Ala Lys Ala Leu Phe Tyr Ser Pro Gln Gln Gly Met Lys
    370                 375                 380
Thr Arg Pro Ala Thr Tyr Asp Pro Gln Asp Ile Leu Asp Ser Cys Pro
385                 390                 395                 400
Ala Ser Tyr Ala Val Cys Val Glu Asp Ser Gly Lys Asp Ser Thr Pro
                405                 410                 415
Gly Ile Leu Ser Thr Pro Lys Tyr Leu Lys Thr Lys Gly Gln Leu Gln
            420                 425                 430
Glu Asp Thr Leu Val Arg Ser Cys Leu Pro Gly Asp Leu Ser Leu Gln
        435                 440                 445
Lys Val Thr Ser Leu Gly Glu Gly Glu Thr Gln Arg Pro Lys Ser Leu
    450                 455                 460
Pro Ser Pro Leu Gly Phe Cys Thr Asp Arg Gly Pro Asp Leu His Thr
465                 470                 475                 480
Leu Arg Ser Glu Glu Pro Glu Thr Pro Arg Tyr Leu Lys Gly Ala Leu
                485                 490                 495
Ser Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Val Ser Leu Pro
            500                 505                 510
Leu His Val His Ser Val Ser Cys Ser Pro Ser Asp Glu Gly Pro Ser
        515                 520                 525
Pro Trp Gly Leu Leu Asp Ser Leu Val Cys Pro Lys Asp Glu Gly Pro
    530                 535                 540
Ala Val Glu Thr Glu Ala Met Cys Pro Ser Ala Ala Ala Ser Glu Leu
```

```
545                 550                 555                 560
Glu Gln Ser Thr Glu Leu Asp Ser Leu Phe Lys Gly Leu Ala Leu Thr
                565                 570                 575
Val Gln Trp Glu Ser
            580


<210> 43
<211> 660
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (1)...(660)

<400> 43
atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca   48
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1               5                  10                  15

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt   96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
            20                  25                  30

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg   144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
        35                  40                  45

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat   192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
    50                  55                  60

aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc   240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65                  70                  75                  80

aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag   288
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
                85                  90                  95

cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att   336
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
            100                 105                 110

att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat   384
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
        115                 120                 125

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act   432
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
    130                 135                 140

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa   480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145                 150                 155                 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag   528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
                165                 170                 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga   576
```

```
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
            180                 185                 190

ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc   624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
        195                 200                 205

tgt gag caa aca acc cat gac gaa acg gtc ccc tcc                   660
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
    210                 215                 220


<210> 44
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 44
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1               5                  10                  15
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
            20                  25                  30
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
        35                  40                  45
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
    50                  55                  60
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65                  70                  75                  80
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
                85                  90                  95
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
            100                 105                 110
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
        115                 120                 125
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
    130                 135                 140
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145                 150                 155                 160
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
                165                 170                 175
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
            180                 185                 190
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
        195                 200                 205
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
    210                 215                 220


<210> 45
<211> 199
<212> PRT
<213> homo sapiens

<400> 45
Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys
 1               5                  10                  15
Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr
            20                  25                  30
Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met
        35                  40                  45
Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly
    50                  55                  60
```

```
Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp
65                  70                  75                  80
Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro
                85                  90                  95
Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe
            100                 105                 110
Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn
        115                 120                 125
Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr
    130                 135                 140
Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg
145                 150                 155                 160
Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
                165                 170                 175
Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
            180                 185                 190
Thr Thr His Asp Glu Thr Val
        195
```

<210> 46
<211> 211
<212> PRT
<213> Homo sapiens

<400> 46

```
Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe
 1                5                  10                  15
Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn
            20                  25                  30
Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile
        35                  40                  45
Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp
    50                  55                  60
Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala
65                  70                  75                  80
Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr
                85                  90                  95
Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val
            100                 105                 110
Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
        115                 120                 125
Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
    130                 135                 140
His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
145                 150                 155                 160
Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
                165                 170                 175
Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
            180                 185                 190
Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
        195                 200                 205
Thr Arg Gln
    210
```

<210> 47
<211> 201
<212> PRT
<213> homo sapiens

<400> 47

```
Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
 1               5                  10                  15
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
            20                  25                  30
Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
        35                  40                  45
Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
    50                  55                  60
Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
65                  70                  75                  80
Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
                85                  90                  95
Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
            100                 105                 110
Gly Met Glu Ile Thr Lys Asp Gly Phe His Leu Val Ile Glu Leu Glu
        115                 120                 125
Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Arg Arg Glu
    130                 135                 140
Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
145                 150                 155                 160
Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
                165                 170                 175
Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr
            180                 185                 190
Glu Cys Val Glu Val Gln Gly Glu Ala
        195                 200
```

<210> 48
<211> 68
<212> PRT
<213> Mus musculus

<400> 48

```
His Thr Thr Val Asp Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln
 1               5                  10                  15
Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser
            20                  25                  30
Thr Ser Asp Thr Val Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg
        35                  40                  45
Lys Trp Leu Ala Lys Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys
    50                  55                  60
Asn Leu Thr Met
65
```

<210> 49
<211> 26
<212> PRT
<213> mus musculus

<400> 49

```
Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys Val Thr Ala Val
 1               5                  10                  15
Ser Ala Gly Gly Pro Pro Val Thr Lys Met
            20                  25
```

<210> 50
<211> 28
<212> PRT
<213> mus musculus

<400> 50
Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Ile Lys Pro Pro Asp
 1   5   10   15
Val Thr Cys Ile Pro Lys Val Arg Ser Ile Gln Met
            20   25

<210> 51
<211> 40
<212> PRT
<213> Mus musculus

<400> 51
Leu Val His Pro Thr Leu Thr Pro Val Leu Ser Glu Asp Gly His Gln
 1   5   10   15
Leu Thr Leu Glu Glu Ile Phe His Asp Leu Phe Tyr Arg Leu Glu Leu
            20   25   30
His Val Asn His Thr Tyr Gln Met
        35   40

<210> 52
<211> 50
<212> PRT
<213> Mus musculus

<400> 52
His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu Thr Pro
 1   5   10   15
Asp Thr Glu Phe Leu Gly Ser Ile Thr Ile Leu Thr Pro Ile Leu Ser
            20   25   30
Lys Glu Ser Ala Pro Tyr Val Cys Arg Val Lys Thr Leu Pro Leu Val
        35   40   45
Pro Arg
    50

<210> 53
<211> 70
<212> PRT
<213> Mus musculus

<400> 53
His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu Thr Pro
 1   5   10   15
Asp Thr Glu Phe His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu
            20   25   30
Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly Ser Ile Thr Ile Leu Thr
        35   40   45
Pro Ile Leu Ser Lys Glu Ser Ala Pro Tyr Val Cys Arg Val Lys Thr
    50   55   60
Leu Pro Leu Val Pro Arg
65   70

<210> 54
<211> 46
<212> PRT
<213> Mus musculus

<400> 54

```
Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys Val Thr Ala Val
 1               5                  10                  15
Ser Ala Gly Gly Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys
            20                  25                  30
Val Thr Ala Val Ser Ala Gly Gly Pro Pro Val Thr Lys Met
        35                  40                  45


<210> 55
<211> 48
<212> PRT
<213> mus musculus

<220>
<221> VARIANT
<222> 6, 11, 13,
<223> Xaa = Any Amino Acid

<400> 55
Thr Asp Arg Phe Ser Xaa Leu Gln His Thr Xaa Ile Xaa Pro Xaa Asp
 1               5                  10                  15
Xaa Xaa Xaa Ile Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Ile
            20                  25                  30
Lys Pro Pro Asp Val Thr Cys Ile Pro Lys Val Arg Ser Ile Gln Met
        35                  40                  45


<210> 56
<211> 92
<212> PRT
<213> homo sapiens

<400> 56
Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser Ser
 1               5                  10                  15
Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro
            20                  25                  30
Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
        35                  40                  45
Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
    50                  55                  60
Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
65                  70                  75                  80
Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met
                85                  90


<210> 57
<211> 28
<212> PRT
<213> Homo sapiens

<400> 57
Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp
 1               5                  10                  15
Val Thr Cys Ile Ser Lys Val Arg Ser Ile Gln Met
            20                  25


<210> 58
<211> 40
<212> PRT
```

<213> Homo sapiens

<400> 58
Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly His Arg
 1   5   10   15
Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu Glu Leu
            20   25   30
Gln Val Asn Arg Thr Tyr Gln Met
        35   40

<210> 59
<211> 25
<212> PRT
<213> Homo sapiens

<400> 59
His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
 1   5   10   15
Asp Thr Glu Phe Leu Gly Thr Ile Met
            20   25

<210> 60
<211> 14
<212> PRT
<213> Homo sapiens

<400> 60
Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr Met
 1   5   10

<210> 61
<211> 12
<212> PRT
<213> Homo sapiens

<400> 61
Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr
 1   5   10

<210> 62
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> A murine IL-22RA soluble receptor with cleavage
      site (Leu Val Pro Arg) remaining on C-Terminus

<400> 62
His Thr Thr Val Asp Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln
 1   5   10   15
Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser
            20   25   30
Thr Ser Asp Thr Val Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg
        35   40   45
Lys Trp Leu Ala Lys Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys
    50   55   60
Asn Leu Thr Met Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys

```
65                  70                  75                  80
Val Thr Ala Val Ser Ala Gly Gly Pro Pro Val Thr Lys Met Thr Asp
                85                  90                  95
Arg Phe Ser Ser Leu Gln His Thr Thr Ile Lys Pro Pro Asp Val Thr
            100                 105                 110
Cys Ile Pro Lys Val Arg Ser Ile Gln Met Leu Val His Pro Thr Leu
        115                 120                 125
Thr Pro Val Leu Ser Glu Asp Gly His Gln Leu Thr Leu Glu Glu Ile
    130                 135                 140
Phe His Asp Leu Phe Tyr Arg Leu Glu Leu His Val Asn His Thr Tyr
145                 150                 155                 160
Gln Met His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu
                165                 170                 175
Thr Pro Asp Thr Glu Phe Leu Gly Ser Ile Thr Ile Leu Thr Pro Ile
            180                 185                 190
Leu Ser Lys Glu Ser Ala Pro Tyr Val Cys Arg Val Lys Thr Leu Pro
        195                 200                 205
Leu Val Pro Arg
    210
```